

TAP - Results

> Job Status

Job ID: 20251103_0427169

Job status: finished!

Log file:

> Results

Summary

Metric	Value and Flag Colour
Total CDR Length	51
CDR Vicinity PSH Score (Kyte & Doolittle)	133.6961
CDR Vicinity PPC Score	1.2523
CDR Vicinity PNC Score	0.3307
SFvCSP Score	3.0

PSH Metric = Patches of Surface Hydrophobicity Metric; PPC Metric = Patches of Positive Charge Metric; PNC Metric = Patches of Negative Charge Metric; SFvCSP = Structural Fv Charge Symmetry Parameter.

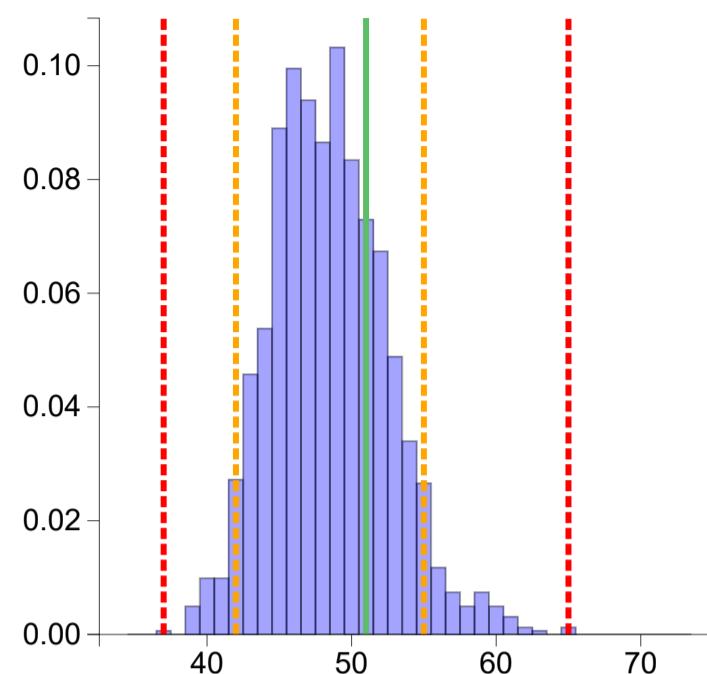
Formulae for each metric are provided in the [TAP paper](#).

Graphical Representations

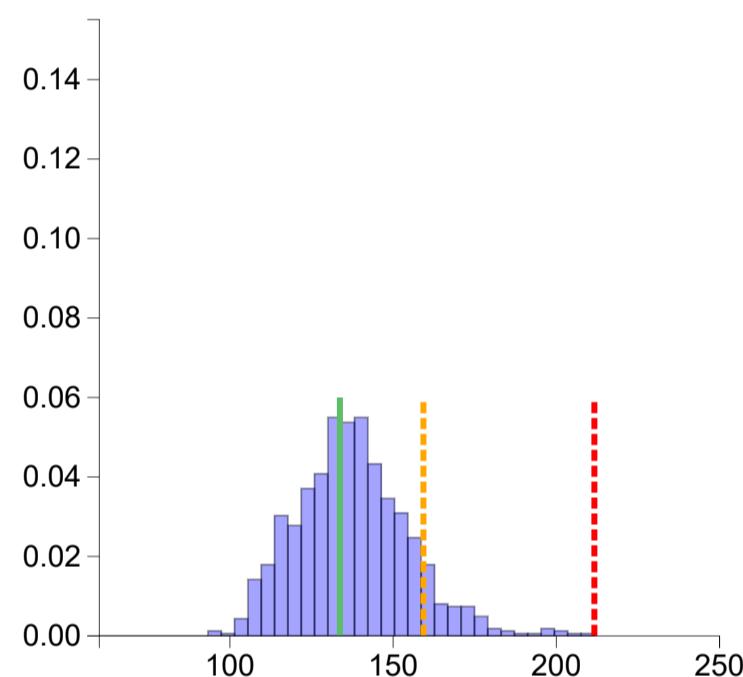
The following histograms show where your antibody sits within the 5 TAP metric distributions of the latest set of 754 post Phase-I therapeutic Fv domains.

Amber and red flag cutoffs are shown by the appropriately-coloured dashed lines, and the value recorded for your antibody is the solid line, coloured by assigned flag.

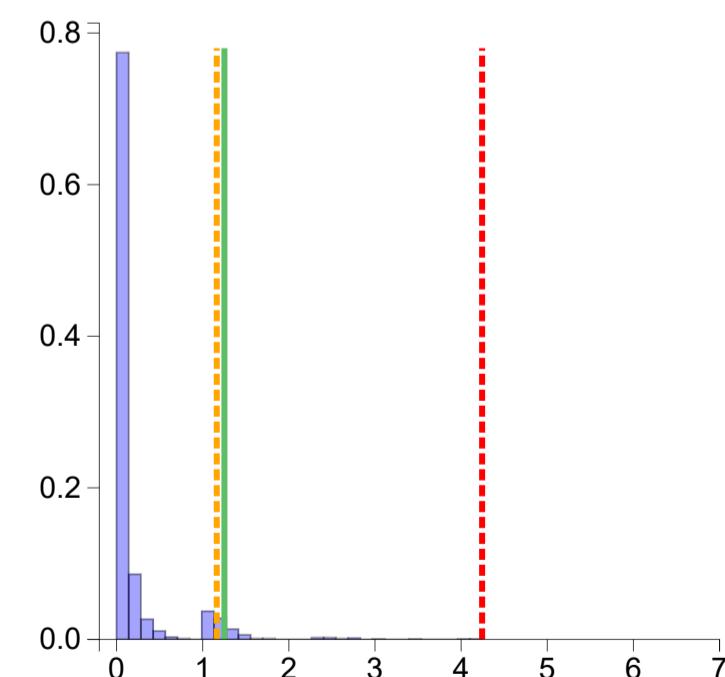
Total CDR Length



PSH Score



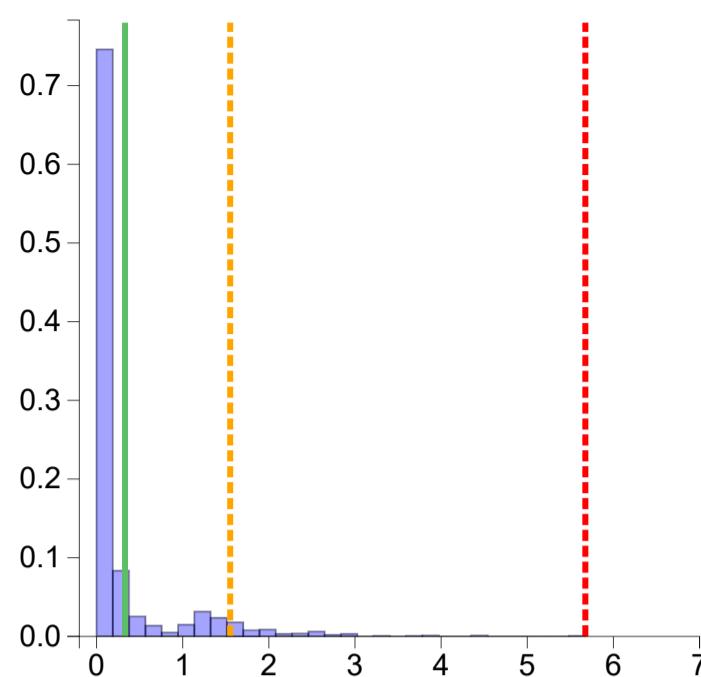
PPC Score



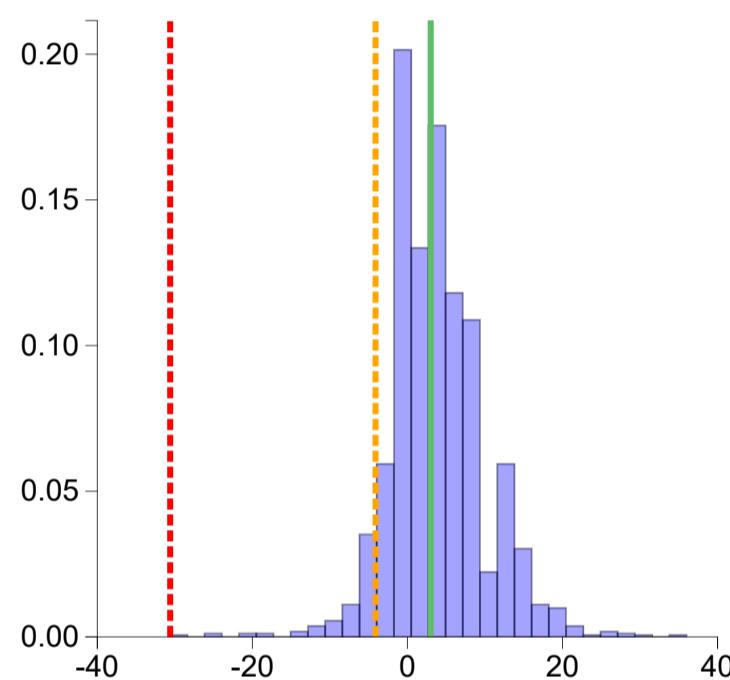
PNC Score

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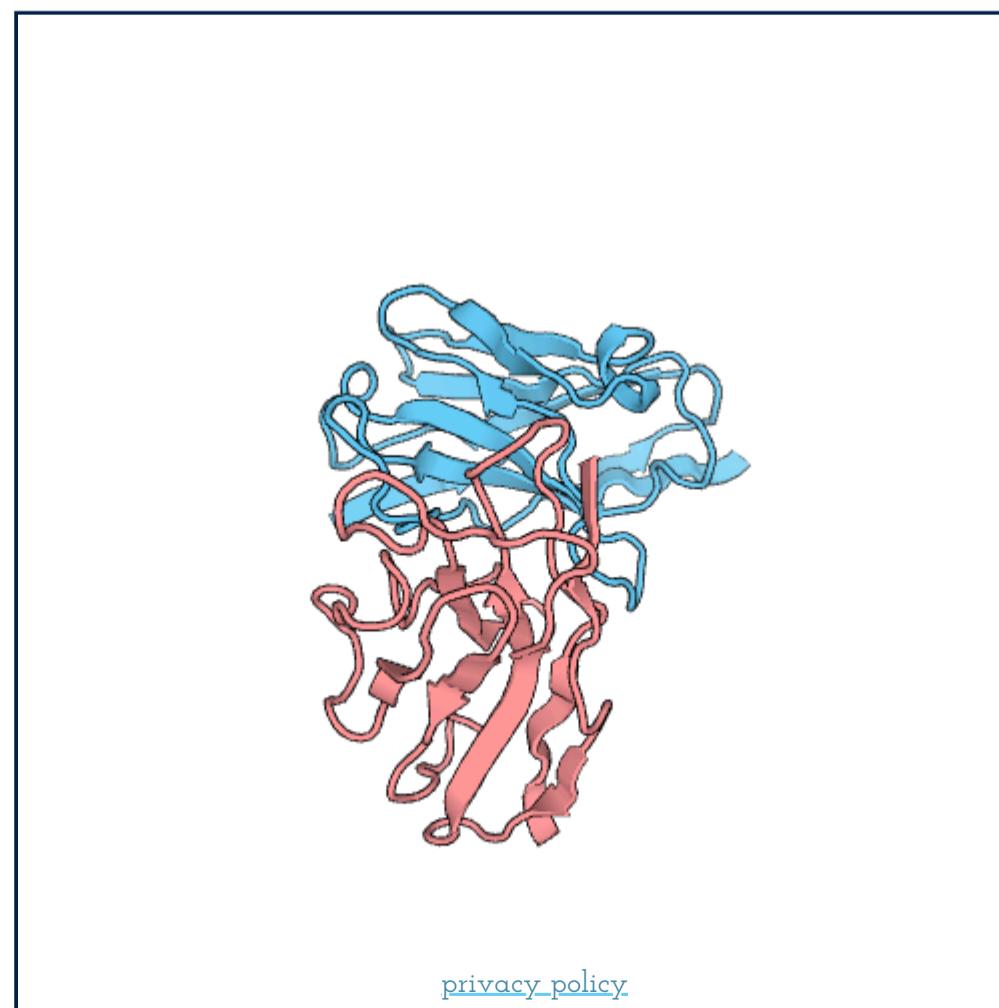
Continue



SFvCSP Score



Model and Visualisation

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Please note the WebGL plugin needs to be enabled to use PV Viewer.
[Continue](#)

Key:

- Heavy Chain
- Light Chain

Display options:

- Heavy & Light Chains
- IMGT CDR Residues
- CDR Vicinity: Hydropobicity
- CDR Vicinity: Positive & Negative Charge

The CDR Vicinity encompasses all **surface-exposed** IMGT CDR and anchor residues, as well as other surface exposed residues with at least one heavy atom within a radius of 4Å. This means that some IMGT CDR residues may not be highlighted (insufficient exposure, < 7.5% relative to Ala-X-Ala for any residue X), whilst some residues outside the IMGT CDR definitions may be highlighted.

To download the model structure, click [here](#).

To view the **estimated quality of the models at residue level** and **sequence liabilities** provided by ABodyBuilder2, please click [here](#).

SAbPred paper: Dunbar, J. et al (2016). Nucleic Acids Res. 44. W474-W478 [[link](#)]



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